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1600

## RAW SEQUENCE LISTING

DATE: 05/07/2002

PATENT APPLICATION: US/09/441,966A

TIME: 14:28:10

Input Set : A:\09-441,966 sequence listing.txt

Output Set: N:\CRF3\05072002\I441966A.raw

p.6

ENTERED

3 <110> APPLICANT: Hall, Roderick L.  
4 Poll, Christopher T.  
5 Newton, Benjamin B.  
6 Taylor, William J.A.  
8 <120> TITLE OF INVENTION: Method For Accelerating The Rate of Mucociliary Clearance  
10 <130> FILE REFERENCE: 98-736-A  
12 <140> CURRENT APPLICATION NUMBER: US 09/441,966A  
13 <141> CURRENT FILING DATE: 1999-11-17  
15 <150> PRIOR APPLICATION NUMBER: US 09/218,913  
16 <151> PRIOR FILING DATE: 1998-12-22  
18 <160> NUMBER OF SEQ ID NOS: 105  
20 <170> SOFTWARE: PatentIn version 3.1  
22 <210> SEQ ID NO: 1  
23 <211> LENGTH: 179  
24 <212> TYPE: PRT  
25 <213> ORGANISM: Homo sapiens  
27 <400> SEQUENCE: 1  
29 Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val  
30 1 5 10 15  
33 Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr  
34 20 25 30  
37 Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser  
38 35 40 45  
41 Asn Asn Tyr Leu Thr Lys Glu Cys Leu Lys Lys Cys Ala Thr Val  
42 50 55 60  
45 Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp  
46 65 70 75 80  
49 Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser  
50 85 90 95  
53 Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr  
54 100 105 110  
57 Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg  
58 115 120 125  
61 Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn  
62 130 135 140  
65 Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln  
66 145 150 155 160  
69 Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly  
70 165 170 175  
73 Ala Val Ser  
77 <210> SEQ ID NO: 2  
78 <211> LENGTH: 197  
79 <212> TYPE: PRT

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80 <213> ORGANISM: Homo sapiens
82 <220> FEATURE:
83 <221> NAME/KEY: SIGNAL
84 <222> LOCATION: (1)..(18)
85 <223> OTHER INFORMATION:
88 <400> SEQUENCE: 2
90 Ala Gly Ser Phe Leu Ala Trp Leu Gly Ser Leu Leu Leu Ser Gly Val
91 1 5 10 15
94 Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser
95 20 25 30
98 Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn
99 35 40 45
102 Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly
103 50 55 60
106 Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala
107 65 70 75 80
110 Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala
111 85 90 95
114 Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp
115 100 105 110
118 His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala
119 115 120 125
122 Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val
123 130 135 140
126 Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn
127 145 150 155 160
130 Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg
131 165 170 175
134 Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu
135 180 185 190
138 Ala Gly Ala Val Ser
139 195
142 <210> SEQ ID NO: 3
143 <211> LENGTH: 153
144 <212> TYPE: PRT
145 <213> ORGANISM: Homo sapiens
147 <400> SEQUENCE: 3
149 Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala
150 1 5 10 15
153 Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu
154 20 25 30
157 Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys
158 35 40 45
161 Glu Glu Cys Leu Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr Gly
162 50 55 60
165 Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser Ala
166 65 70 75 80
169 Pro Arg Arg Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn Tyr
170 85 90 95

```

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```

173 Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser
174           100           105           110
177 Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe
178           115           120           125
181 Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu
182           130           135           140
185 Ala Cys Met Leu Arg Cys Phe Arg Gln
186 145           150
189 <210> SEQ ID NO: 4
190 <211> LENGTH: 58
191 <212> TYPE: PRT
192 <213> ORGANISM: Homo sapiens
194 <400> SEQUENCE: 4
196 Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala
197 1           5           10           15
200 Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu
201           20           25           30
204 Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys
205           35           40           45
208 Glu Glu Cys Leu Lys Lys Cys Ala Thr Val
209           50           55
212 <210> SEQ ID NO: 5
213 <211> LENGTH: 51
214 <212> TYPE: PRT
215 <213> ORGANISM: Homo sapiens
217 <400> SEQUENCE: 5
219 Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg
220 1           5           10           15
223 Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly
224           20           25           30
227 Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu
228           35           40           45
231 Lys Lys Cys
232           50
235 <210> SEQ ID NO: 6
236 <211> LENGTH: 58
237 <212> TYPE: PRT
238 <213> ORGANISM: Homo sapiens
240 <400> SEQUENCE: 6
242 Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala
243 1           5           10           15
246 Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn
247           20           25           30
250 Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu
251           35           40           45
254 Glu Ala Cys Met Leu Arg Cys Phe Arg Gln
255           50           55
258 <210> SEQ ID NO: 7
259 <211> LENGTH: 51

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260 <212> TYPE: PRT
261 <213> ORGANISM: Homo sapiens
263 <400> SEQUENCE: 7
265 Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg
266 1          5          10          15
269 Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly
270          20          25          30
273 Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met
274          35          40          45
277 Leu Arg Cys
278          50
281 <210> SEQ ID NO: 8
282 <211> LENGTH: 92
283 <212> TYPE: PRT
284 <213> ORGANISM: Homo sapiens
286 <400> SEQUENCE: 8
288 Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
289 1          5          10          15
292 Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr
293          20          25          30
296 Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser
297          35          40          45
300 Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val
301          50          55          60
304 Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp
305 65          70          75          80
308 Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser
309          85          90
312 <210> SEQ ID NO: 9
313 <211> LENGTH: 708
314 <212> TYPE: DNA
315 <213> ORGANISM: Artificial Sequence
317 <220> FEATURE:
318 <223> OTHER INFORMATION: Consensus DNA sequence of human Bikunin (Fig. 3).
320 <220> FEATURE:
321 <221> NAME/KEY: misc_feature
322 <222> LOCATION: (679)..(679)
323 <223> OTHER INFORMATION: "n" is any nucleotide.
326 <220> FEATURE:
327 <221> NAME/KEY: misc_feature
328 <222> LOCATION: (707)..(707)
329 <223> OTHER INFORMATION: "n" is any nucleotide.
332 <400> SEQUENCE: 9
333 ggccggggtcg tttctgcct ggctgggata gctgctcctc tctgggggtcc tggcggccga      60
335 ccgagaacgc agcatccacg acttctgcct ggtgtcgaa gttgtgggca gatgccgggc      120
337 ctccatgcct aggtggtggt acaatgtcac tgacggatcc tgccagctgt ttgtgtatgg      180
339 gggctgtgac ggaaacagca ataattacct gaccaaggag gagtgcctca agaaatgtgc      240
341 cactgtcaca gagaatgcc cgggtgacct ggccaccagc aggaatgcag cggattcctc      300
343 tgtcccaagt gctcccagaa ggcaggattc tgaagaccac tccagcgata tgttcaacta      360

```

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Input Set : A:\09-441,966 sequence listing.txt

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345 tgaagaatac tgcaccgcca acgcagtcac tgggccttgc cgtgcatacct tcccacgctg 420  
 347 gtactttgac gtggagagga actcctgcaa taacttcatac tatggaggct gccggggcaa 480  
 349 taagaacagc taccgctctg aggaggcctg catgctccgc tgcttccgcc agcaggagaa 540  
 351 tcctccccctg ccccttggt caaagggtggg ggttctggcc ggggctgttt cgtgatggtg 600  
 353 ttgatccttt tcctggggag catccatggt ctactgatt ccgggtggca aggaggaacc 660  
 355 **aggagcgtgc cctgcgganc gtctggagct tcggagatga caagggnt** 708  
 358 <210> SEQ ID NO: 10  
 359 <211> LENGTH: 197  
 360 <212> TYPE: PRT  
 361 <213> ORGANISM: Artificial Sequence  
 363 <220> FEATURE:  
 364 <223> OTHER INFORMATION: Amino acids -18 to 179 of translation of consensus sequence  
 in Fig. 3.  
 366 <400> SEQUENCE: 10  
 368 Ala Gly Ser Phe Leu Ala Trp Leu Gly Ser Leu Leu Leu Ser Gly Val  
 369 1 5 10 15  
 372 Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser  
 373 20 25 30  
 376 Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn  
 377 35 40 45  
 380 Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly  
 381 50 55 60  
 384 Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala  
 385 65 70 75 80  
 388 Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala  
 389 85 90 95  
 392 Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp  
 393 100 105 110  
 396 His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala  
 397 115 120 125  
 400 Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val  
 401 130 135 140  
 404 Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn  
 405 145 150 155 160  
 408 Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg  
 409 165 170 175  
 412 Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu  
 413 180 185 190  
 416 Ala Gly Ala Val Ser  
 417 195  
 420 <210> SEQ ID NO: 11  
 421 <211> LENGTH: 179  
 422 <212> TYPE: PRT  
 423 <213> ORGANISM: Artificial Sequence  
 425 <220> FEATURE:  
 426 <223> OTHER INFORMATION: Variants of human Bikunin.  
 428 <220> FEATURE:  
 429 <221> NAME/KEY: MISC\_FEATURE  
 430 <222> LOCATION: (8)..(8)  
 431 <223> OTHER INFORMATION: Each "Xaa" independently represents a naturally occurring  
 amino

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/441,966A

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 679,707  
Seq#:11; Xaa Pos. 8,17,19,21,22,23,24,25,26,40,42,45,46,47,52,64,103,112  
Seq#:11; Xaa Pos. 114,116,117,118,119,120,121,135,137,140,141,142,147,159  
Seq#:12; N Pos. 361,367,384,390  
Seq#:14; N Pos. 424,481,509  
Seq#:16; N Pos. 3,11,12,17,48,425  
Seq#:17; N Pos. 6,401,407  
Seq#:48; N Pos. 1358  
Seq#:51; N Pos. 46,117,313  
Seq#:72; Xaa Pos. 9,11,17,19  
Seq#:74; Xaa Pos. 25  
Seq#:75; N Pos. 425,482,510  
Seq#:76; Xaa Pos. 25  
Seq#:77; N Pos. 45,49,118,231,305  
Seq#:78; N Pos. 117,123,321  
Seq#:79; N Pos. 9,11,222,231,262,267,274  
Seq#:80; N Pos. 44,46,76,114,187,268,309,317,332,370  
Seq#:81; N Pos. 35,148,235,261,272,293,300,313,320  
Seq#:82; N Pos. 56,137,145,159,233  
Seq#:83; N Pos. 20,26,95,292,313,314,315  
Seq#:84; N Pos. 27,139,223,232,302,310,322,328,357,375,392,398,405,427,437  
Seq#:84; N Pos. 449,458,474  
Seq#:85; N Pos. 361,367,384,390  
Seq#:86; N Pos. 3,11,12,17,48,425  
Seq#:87; N Pos. 7,403,409  
Seq#:88; N Pos. 48,62,211,232,245,309,318  
Seq#:89; N Pos. 424,481,509  
Seq#:90; N Pos. 257  
Seq#:91; N Pos. 19,147  
Seq#:92; N Pos. 33,55,213,228,259,267,324,333,344,387  
Seq#:93; N Pos. 306,328,342,365,370,377,382,402  
Seq#:94; N Pos. 1,142,339,347  
Seq#:95; N Pos. 334,368,376  
Seq#:96; N Pos. 108,261  
Seq#:97; N Pos. 20,30  
Seq#:98; N Pos. 45,102,105,159,174,213,337  
Seq#:100; N Pos. 304,309  
Seq#:101; N Pos. 24  
Seq#:102; N Pos. 61,74,122,184  
Seq#:103; N Pos. 7  
Seq#:104; N Pos. 32,67,136  
Seq#:105; N Pos. 13,19,107